Amendments to the Specification:

Please replace page 35, lines 8-10 with the following lines:

practical approach. Schena M. Oxford University Press 1999" and the World

Wide Web, ~~(http://cmgm.standford.edu/pbrown/protocols/index.html)~~,

~~http://arrayit.com/DNA-Microarray-Protocols/)~~ and specialized distributors (e.g.,

Affymetrix).

Please replace page 37, lines 21-24 with the following lines:

The obtained sequence (SEQ ID NO:1) has a putative open reading frame of 259

amino acids (SEQ ID NO:2). The deduced protein sequence was submitted to

prediction algorithms for cellular localization using PSORT program and TopPred

program. ~~(PSORT: http://psort.nibb.ac.jp/ and TopPred:~~

~~http//www.biokemi.su.se/~server/toppred2/toppred_source.html~~). It is predicted to

have

Please replace page 43, lines 12-22 with the following lines:

The HLA-A2 binding peptide sequences are predicted either by the Parker's

algorithm (Parker, K. C., M.A. Bednarek, and J.E. Coligan, 1994. Scheme for

ranking potential HLA-A2 binding peptides based on independent binding of

individual peptide sidechains. J. Immunol. 152:163 ~~and~~

~~http://bimas.dcrt.nih.gov/molbio/hla_bind/~~) or the Rammensee method

(Rammensee, Friede, Stevanovic, MHC ligands and peptide motifs: 1st listing,

Immunogenetics 41, 178-228, 1995; Rammensee, Bachman Stevanovic: MAHC

ligand and peptide motifs. Landes Bioscience 1997~~, and~~

~~http://134.2.96.221/scripts/hlaserver.dll/home.htm~~). Peptides are then screened in

the HLA-A2.1/Kb transgenic mice model (Vitiello et al.). The sequence used to

perform the prediction is EPHB2v, as it is identical to EPHB2 with an additional

C-terminal sequence extension.